

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2277 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 166..1755
- (D) OTHER INFORMATION: /product= "ALPHA-2 SUBUNIT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CAATGACCTG TTTTCTTCTG TAACCACAGG TTCGGTGGTG AGAGGAASCY TCGCAGAATC	60
CAGCAGAATC CTCACAGAAT CCAGCAGCAG CTCTGCTGGG GACATGGTCC ATGGTGCAAC	120
CCACAGCAAA GCCCTGACCT GACCTCCTGA TGCTCAGGAG AAGCCATGGG CCGCTCCTGT	180
CCTGTGTTCC TGTCTTCAC AAAGCTCAGC CTGTGGTGGC TCCTTCTGAC CCCAGCAGGT	240
GGAGAGGAAG CTAAGCGCCC ACCTCCCAGG GCTCCTGGAG ACCCACTCTC CTCTCCCAGT	300
CCCACGGCAT TGCCGCAGGG AGGCTCGCAT ACCGAGACTG AGGACCGGCT CTTCAAACAC	360
CTCTCCGGG GCTACAACCG CTGGGCGCGC CCGGTGCCCA ACACTTCAGA CGTGGTGATT	420
GTGCGCTTTG GACTGTCCAT CGCTCAGCTC ATCGATGTGG ATGAGAAGAA CCAAATGATG	480
ACCACCAACG TCTGGCTAA ACAGGAGTGG AGCGACTACA AACTGCGCTG GAACCCCGCT	540
GATTTTGGCA ACATCACATC TCTCAGGGTC CTTTCTGAGA TGATCTGGAT CCCCACATT	600
GTTCTCTACA ACAATGCAGA TGGGGAGTTT GCAGTGACCC ACATGACCAA GGCCACCTC	660
TTCTCCACGG GCACTGTGCA CTGGGTGCCC CCGGCCATCT ACAAGAGCTC CTGCAGCATC	720
GACGTCACCT TCTTCCCCTT CGACCAGCAG AACTGCAAGA TGAAGTTTGG CTCCTGGACT	780
TATGACAAGG CCAAGATCGA CCTGGAGCAG ATGGAGCAGA CTGTGGACCT GAAGGACTAC	840
TGGGAGAGCG GCGAGTGGGC CATCGTCAAT GCCACGGCA CCTACAACAG CAAGAAGTAC	900
GACTGCTGCG CCGAGATCTA CCCCACGTC ACCTACGCTT TCGTCATCCG GCGGCTGCCG	960
CTCTTCTACA CCATCAACCT CATCATCCCC TGCCTGCTCA TCTCCTGCCT CACTGTGCTG	1020
GTCTTCTACC TGCCCTCCGA CTGCGGCGAG AAGATCACGC TGTGCATTTC GGTGCTGCTG	1080
TCACTCACCG TCTTCTGCT GTCATCACT GAGATCATCC CGTCCACCTC GCTGGTCATC	1140
CCGCTCATCG GCGAGTACCT GCTGTTACCC ATGATCTTCG TCACCCTGTC CATCGTCATC	1200
ACCGTCTTCG TGCTCAATGT GCACCACCGC TCCCCAGCA CCCACACCAT GCCCCACTGG	1260
GTGCGGGGGG CCCTTCTGGG CTGTGTGCCC CGGTGGCTTC TGATGAACCG GCCCCACCA	1320
CCCGTGGAGC TCTGCCACCC CCTACGCTG AAGCTCAGCC CCTCTTATCA CTGGCTGGAG	1380
AGCAACGTGG ATGCCGAGGA GAGGGAGGTG GTGGTGGAGG AGGAGGACAG ATGGGCATGT	1440

GCAGGTCATG TGGCCCCCTC TGTGGGCACC CTCTGCAGCC ACGGCCACCT GCACTCTGGG 1500  
 GCCTCAGGTC CCAAGGCTGA GGCTCTGCTG CAGGAGGGTG AGCTGCTGCT ATCACCCAC 1560  
 ATGCAGAAGG CACTGGAAGG TGTGCACTAC ATTGCCGACC ACCTGCGGTC TGAGGATGCT 1620  
 GACTCTTCGG TGAAGGAGGA CTGGAAGTAT GTTGCCATGG TCATCGACAG GATCTTCCTC 1680  
 TGGCTGTTTA TCATCGTCTG CTTCTGGGG ACCATCGGCC TCTTTCTGCC TCCGTTCTTA 1740  
 GCTGGAATGA TCTGACTGCA CCTCCCTCGA GCTGGCTCCC AGGGCAAAGG GGAGGGTTCT 1800  
 TGGATGTGGA AGGGCTTTGA ACAATGTTTA GATTTGGAGA TGAGCCCAA GTGCCAGGGA 1860  
 GAACAGCCAG GTGAGGTGGG AGGTTGAGA GCCAGGTGAG GTCTCTCTAA GTCAGGCTGG 1920  
 GGTGAAGTT TGGAGTCTGT CCGAGTTTC AGGGTGCTGA GCTGTATGGT CCAGCAGGGG 1980  
 AGTAATAAGG GCTCTTCCGG AAGGGGAGGA AGCGGGAGGC AGGGCCTGCA CCTGATGTGG 2040  
 AGGTACAGGG CAGATCTTCC CTACCGGGGA GGGATGGATG GTTGGATACA GGTGGCTGGG 2100  
 CTATTCCATC CATCTGGAAG CACATTGAG CCTCCAGGCT TCTCCTTGAC GTCATTCTC 2160  
 TCCTTCCTTG CTCCAAATG GCTCTGCACC AGCGGGCCCC CAGGAGGTCT GGCAGAGCTG 2220  
 AGAGCCATGG CCTGCAGGGG CTCCATATGT CCTACGCGT GCAGCAGGCA AACAAGA 2277

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 529 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Gly	Pro	Ser	Cys	Pro	Val	Phe	Leu	Ser	Phe	Thr	Lys	Leu	Ser	Leu
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Trp	Trp	Leu	Leu	Leu	Thr	Pro	Ala	Gly	Gly	Glu	Glu	Ala	Lys	Arg	Pro
		20						25					30		
Pro	Pro	Arg	Ala	Pro	Gly	Asp	Pro	Leu	Ser	Ser	Pro	Ser	Pro	Thr	Ala
		35					40					45			
Leu	Pro	Gln	Gly	Gly	Ser	His	Thr	Glu	Thr	Glu	Asp	Arg	Leu	Phe	Lys
	50					55					60				
His	Leu	Phe	Arg	Gly	Tyr	Asn	Arg	Trp	Ala	Arg	Pro	Val	Pro	Asn	Thr
	65				70				75					80	
Ser	Asp	Val	Val	Ile	Val	Arg	Phe	Gly	Leu	Ser	Ile	Ala	Gln	Leu	Ile
			85					90						95	
Asp	Val	Asp	Glu	Lys	Asn	Gln	Met	Met	Thr	Thr	Asn	Val	Trp	Leu	Lys
		100					105						110		
Gln	Glu	Trp	Ser	Asp	Tyr	Lys	Leu	Arg	Trp	Asn	Pro	Ala	Asp	Phe	Gly
		115					120					125			
Asn	Ile	Thr	Ser	Leu	Arg	Val	Pro	Ser	Glu	Met	Ile	Trp	Ile	Pro	Asp
	130					135					140				





[illegible][illegible][illegible]



CCCACTCATC GCGAGTACC TGCTGTTAC CATGATCTT GTCACCTGT CCATCGCCAT	1140
CACGGTCTTC GTGCTCAACG TGCACCACCG CTCGCCACGC ACGCACACCA TGCCACCTG	1200
GGTACGCAGG GTCTTCCTGG ACATCGTGCC ACGCCTGCTC CTCATGAAGC GGCCGTCCGT	1260
GGTCAAGGAC AATTGCCGGC GGCTCATCGA GTCCATGCAT AAGATGGCCA GTGCCCCGCG	1320
CTTCTGGCCC GAGCCAGAAG GGGAGCCCCC TGCCACGAGC GGCACCCAGA GCCTGCACCC	1380
TCCCTCACCG TCCTTCTGCG TCCCCCTGGA TGTGCCGGCT GAGCCTGGGC CTTCCTGCAA	1440
GTCACCTCC GACCAGCTCC CTCCTCAGCA GCCCCTGGAA GCTGAGAAAG CCAGCCCCCA	1500
CCCCTCGCCT GGACCTGCC GCGCGCCCCA CGGCACCCAG GCACCAGGGC TGGCCAAAGC	1560
CAGGTCCCTC AGCGTCCAGC ACATGTCCAG CCCTGGCGAA GCGGTGGAAG GCGGCGTCCG	1620
GTGCCGGTCT CGGAGCATCC AGTACTGTGT TCCCGGAGAC GATGCCGCC CCGAGGCAGA	1680
TGGCCAGGCT GCGGCGCCCC TGGCCTCTCG CAACAGCCAC TCGGCTGAGC TCCCACCCCC	1740
AGACCAGCCC TCTCCGTGCA AATGCACATG CAAGAAGGAG CCCTCTTCGG TGTCCCCGAG	1800
CGCCACGGTC AAGACCCGCA GCACCAAAGC GCGCGCGCCG CACCTGCCCC TGTGCGCGGC	1860
CCTGAGCCCG GCGGTGGAGG GCGTCCAGTA CATTGCAGAC CACCTGAAG CCGAAGACAC	1920
AGACTTCTCG GTGAAGGAGG ACTGGAAGTA CGTGCCCATG GTCATCGACC GCATCTTCT	1980
CTGGATGTTT ATCATCGTCT GCCTGCTGGG GACGGTGGGC CTCTTCCTGC CGCCCTGGCT	2040
GGCTGGCATG ATCTAGGAAG GGACCGGGAG CCTGCGTGGC CTGGGGCTGC CGYGCACGGG	2100
GCCAGCATCC ATGCGGCCGG CCTGGGGCCG GGCTGGCTTC TCCCTGGACT CTGTGGGGCC	2160
ACACGTTTGC CAAATTTTCC TTCCTGTCTT GTGTCTGCTG TAAGACGGCC TTGGACGGCG	2220
ACACGGCCTC TGGGGAGACC GAGTGTGGAG CTGCTTCCAG TTGGACTCTS GCCTCAGNAG	2280
GCAGCGGCTT GGAGCAGAGG TGGCGGTGCG CGCCTYCTAC CTGCAGGACT CGGGCTAAGT	2340
CCAGCTCTCC CCCTGCGCAG CCC	2363

(2) INFORMATION FOR SEQ ID NO:6:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 627 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Glu	Leu	Gly	Gly	Pro	Gly	Ala	Pro	Arg	Leu	Leu	Pro	Pro	Leu	Leu	
1				5					10					15		
Leu	Leu	Leu	Gly	Thr	Gly	Leu	Leu	Arg	Ala	Ser	Ser	His	Val	Glu	Thr	
			20					25					30			
Arg	Ala	His	Ala	Glu	Glu	Arg	Leu	Leu	Lys	Lys	Leu	Phe	Ser	Gly	Tyr	
		35					40				45					
Asn	Lys	Trp	Ser	Arg	Pro	Val	Ala	Asn	Ile	Ser	Asp	Val	Val	Leu	Val	
	50					55					60					

Arg 65	Phe	Gly	Leu	Ser	Ile 70	Ala	Gln	Leu	Ile	Asp 75	Val	Asp	Glu	Lys	Asn 80
Gln	Met	Met	Thr	Thr 85	Asn	Val	Trp	Val	Lys 90	Gln	Glu	Trp	His	Asp 95	Tyr
Lys	Leu	Arg	Trp 100	Asp	Pro	Ala	Asp	Tyr 105	Glu	Asn	Val	Thr	Ser 110	Ile	Arg
Ile	Pro	Ser 115	Glu	Leu	Ile	Trp	Arg 120	Pro	Asp	Ile	Ala	Leu	Tyr 125	Asn	Asn
Ala	Asp 130	Gly	Asp	Phe	Ala	Ala 135	Thr	His	Leu	Thr	Lys 140	Ala	His	Leu	Phe
His 145	Asp	Gly	Arg	Val	Gln 150	Arg	Thr	Pro	Pro	Ala 155	Ile	Tyr	Lys	Ser	Ser 160
Cys	Ser	Ile	Asp	Val 165	Thr	Phe	Phe	Pro	Phe 170	Asp	Gln	Gln	Asn 175	Cys	Thr
Met	Lys	Phe 180	Gly	Ser	Trp	Thr	Tyr	Asp 185	Lys	Ala	Lys	Ile	Asp 190	Leu	Val
Asn	Met	His 195	Ser	Arg	Val	Asp	Gln 200	Leu	Asp	Phe	Trp	Glu 205	Ser	Gly	Glu
Trp	Leu 210	Ile	Ser	Asp	Ala	Val 215	Gly	Thr	Tyr	Asn	Thr 220	Arg	Lys	Tyr	Glu
Cys 225	Cys	Ala	Glu	Ile	Tyr 230	Pro	Asp	Ile	Thr	Tyr 235	Ala	Tyr	Ala	Ile	Arg 240
Arg	Leu	Pro	Leu	Phe 245	Tyr	Thr	Ile	Asn	Leu 250	Ile	Ile	Pro	Trp	Leu 255	Leu
Ile	Ser	Cys	Leu 260	Thr	Ala	Leu	Val	Phe 265	Tyr	Leu	Pro	Ser	Glu 270	Cys	Gly
Glu	Lys	Ile 275	Thr	Leu	Cys	Ile	Ser 280	Val	Leu	Leu	Ser	Leu 285	Thr	Val	Phe
Leu 290	Leu	Leu	Ile	Thr	Glu	Ile 295	Ile	Pro	Ser	Thr	Ser 300	Leu	Val	Ile	Pro
Leu 305	Ile	Gly	Glu	Tyr	Leu 310	Leu	Phe	Thr	Met	Ile 315	Phe	Val	Thr	Leu	Ser 320
Ile	Ala	Ile	Thr	Val 325	Phe	Val	Leu	Asn	Val 330	His	His	Arg	Ser	Pro 335	Arg
Thr	His	Thr	Met 340	Pro	Thr	Trp	Val	Arg 345	Arg	Val	Phe	Leu	Asp 350	Ile	Val
Pro	Arg	Leu 355	Leu	Leu	Met	Lys	Arg 360	Pro	Ser	Val	Val	Lys 365	Asp	Asn	Cys
Arg 370	Arg	Leu	Ile	Glu	Ser	Met 375	His	Lys	Met	Ala	Ser 380	Ala	Pro	Arg	Phe
Trp 385	Pro	Glu	Pro	Glu	Gly 390	Glu	Pro	Pro	Ala	Thr 395	Ser	Gly	Thr	Gln	Ser 400
Leu	His	Pro	Pro	Ser 405	Pro	Ser	Phe	Cys 410	Val	Pro	Leu	Asp	Val	Pro 415	Ala



Glu Pro Gly Pro Ser Cys Lys Ser Pro Ser Asp Gln Leu Pro Pro Gln  
 420 425 430  
 Gln Pro Leu Glu Ala Glu Lys Ala Ser Pro His Pro Ser Pro Gly Pr  
 435 440 445  
 Cys Arg Pro Pro His Gly Thr Gln Ala Pro Gly Leu Ala Lys Ala Arg  
 450 455 460  
 Ser Leu Ser Val Gln His Met Ser Ser Pro Gly Glu Ala Val Glu Gly  
 465 470 475 480  
 Gly Val Arg Cys Arg Ser Arg Ser Ile Gln Tyr Cys Val Pro Arg Asp  
 485 490 495  
 Asp Ala Ala Pro Glu Ala Asp Gly Gln Ala Ala Gly Ala Leu Ala Ser  
 500 505 510  
 Arg Asn Ser His Ser Ala Glu Leu Pro Pro Pro Asp Gln Pro Ser Pro  
 515 520 525  
 Cys Lys Cys Thr Cys Lys Lys Glu Pro Ser Ser Val Ser Pro Ser Ala  
 530 535 540  
 Thr Val Lys Thr Arg Ser Thr Lys Ala Pro Pro Pro His Leu Pro Leu  
 545 550 555 560  
 Ser Pro Ala Leu Ser Arg Ala Val Glu Gly Val Gln Tyr Ile Ala Asp  
 565 570 575  
 His Leu Lys Ala Glu Asp Thr Asp Phe Ser Val Lys Glu Asp Trp Lys  
 580 585 590  
 Tyr Val Ala Met Val Ile Asp Arg Ile Phe Leu Trp Met Phe Ile Ile  
 595 600 605  
 Val Cys Leu Leu Gly Thr Val Gly Leu Phe Leu Pro Pro Trp Leu Ala  
 610 615 620  
 Gly Met Ile  
 625

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1828 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 155..1561
- (D) OTHER INFORMATION: /product= "ALPHA-5 SUBUNIT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CCCGCGCGGA GCTGTGGCGC GGAGCGGCCC CGCTGCTGCG TGTGCCCTCG TTTGTCTCA	60
CGACTCACAC TCAGTGCTGC ATTCCCCAAG AGTTCGCGTT CCCCAGCGCG CGGTGAGAG	120
GCGGCTGCCC GCGGTCCCGC GCGGGCGCGG GGCG ATG GCG GCG CGG GGG TCA	172
Met Ala Ala Arg Gly Ser	
1 5	

GGG CCC CGC GCG CTC CGC CTG CTG CTC TTG GTC CAG CTG GTC GCG GGG Gly Pro Arg Ala Leu Arg Leu L u Leu Leu Val Gln Leu Val Ala Gly	220
CGC TGC GGT CTA GCG GGC GCG GCG GCG GCG GCG CAG AGA GGA TTA TCT Arg Cys Gly Leu Ala Gly Ala Ala Gly Gly Ala Gln Arg Gly Leu Ser	268
GAA CCT TCT TCT ATT GCA AAA CAT GAA GAT AGT TTG CTT AAG GAT TTA Glu Pro Ser Ser Ile Ala Lys His Glu Asp Ser Leu Leu Lys Asp Leu	316
TTT CAA GAC TAC GAA AGA TGG GTT CGT CCT GTG GAA CAC CTG AAT GAC Phe Gln Asp Tyr Glu Arg Trp Val Arg Pro Val Glu His Leu Asn Asp	364
AAA ATA AAA ATA AAA TTT GGA CTT GCA ATA TCT CAA TTG GTG GAT GTG Lys Ile Lys Ile Lys Phe Gly Leu Ala Ile Ser Gln Leu Val Asp Val	412
GAT GAG AAA AAT CAG TTA ATG ACA ACA AAC GTC TGG TTG AAA CAG GAA Asp Glu Lys Asn Gln Leu Met Thr Thr Asn Val Trp Leu Lys Gln Glu	460
TGG ATA GAT GTA AAA TTA AGA TGG AAC CCT GAT GAC TAT GGT GGA ATA Trp Ile Asp Val Lys Leu Arg Trp Asn Pro Asp Asp Tyr Gly Gly Ile	508
AAA GTT ATA CGT GTT CCT TCA GAC TCT GTC TGG ACA CCA GAC ATC GTT Lys Val Ile Arg Val Pro Ser Asp Ser Val Trp Thr Pro Asp Ile Val	556
TTG TTT GAT AAT GCA GAT GGA CGT TTT GAA GGG ACC AGT ACG AAA ACA Leu Phe Asp Asn Ala Asp Gly Arg Phe Glu Gly Thr Ser Thr Lys Thr	604
GTC ATC AGG TAC AAT GGC ACT GTC ACC TGG ACT CCA CCG GCA AAC TAC Val Ile Arg Tyr Asn Gly Thr Val Thr Trp Thr Pro Pro Ala Asn Tyr	652
AAA AGT TCC TGT ACC ATA GAT GTC ACG TTT TTC CCA TTT GAC CTT CAG Lys Ser Ser Cys Thr Ile Asp Val Thr Phe Phe Pro Phe Asp Leu Gln	700
AAC TGT TCC ATG AAA TTT GGT TCT TGG ACT TAT GAT GGA TCA CAG GTT Asn Cys Ser Met Lys Phe Gly Ser Trp Thr Tyr Asp Gly Ser Gln Val	748
GAT ATA ATT CTA GAG GAC CAA GAT GTA GAC AAG AGA GAT TTT TTT GAT Asp Ile Ile Leu Glu Asp Gln Asp Val Asp Lys Arg Asp Phe Phe Asp	796
AAT GGA GAA TGG GAG ATT GTG AGT GCA ACA GGG AGC AAA GGA AAC AGA Asn Gly Glu Trp Glu Ile Val Ser Ala Thr Gly Ser Lys Gly Asn Arg	844
ACC GAC AGC TGT TGC TGG TAT CCG TAT GTC ACT TAC TCA TTT GTA ATC Thr Asp Ser Cys Cys Trp Tyr Pro Tyr Val Thr Tyr Ser Phe Val Ile	892
AAG CGC CTG CCT CTC TTT TAT ACC TTG TTC CTT ATA ATA CCC TGT ATT Lys Arg Leu Pro Leu Phe Tyr Thr Leu Phe Leu Ile Ile Pro Cys Ile	940
GGG CTC TCA TTT TTA ACT GTA CTT GTC TTC TAT CTT CCT TCA AAT GAA Gly Leu Ser Phe Leu Thr Val Leu Val Ph Tyr Leu Pro Ser Asn Glu	988

00703044 = 1566260

GGT GAA AAG ATT TGT CTC TGC ACT TCA GTA CTT GTG TCT TTG ACT GTC Gly Glu Lys Ile Cys Leu Cys Thr Ser Val Leu Val Ser Leu Thr Val 280 285 290	1036
TTC CTT CTG GTT ATT GAA GAG ATC ATA CCA TCA TCT TCA AAA GTC ATA Phe Leu Leu Val Ile Glu Glu Ile Ile Pro Ser Ser Ser Lys Val Ile 295 300 305 310	1084
CCT CTA ATT GGA GAG TAT CTG GTA TTT ACC ATG ATT TTT GTG ACA CTG Pro Leu Ile Gly Glu Tyr Leu Val Phe Thr Met Ile Phe Val Thr Leu 315 320 325	1132
TCA ATT ATG GTA ACC GTC TTC GCT ATC AAC ATT CAT CAT CGT TCT TCC Ser Ile Met Val Thr Val Phe Ala Ile Asn Ile His His Arg Ser Ser 330 335 340	1180
TCA ACA CAT AAT GCC ATG GCG CCT TTG GTC CGC AAG ATA TTT CTT CAC Ser Thr His Asn Ala Met Ala Pro Leu Val Arg Lys Ile Phe Leu His 345 350 355	1228
ACG CTT CCC AAA CTG CTT TGC ATG AGA AGT CAT GTA GAC AGG TAC TTC Thr Leu Pro Lys Leu Leu Cys Met Arg Ser His Val Asp Arg Tyr Phe 360 365 370	1276
ACT CAG AAA GAG GAA ACT GAG AGT GGT AGT GGA CCA AAA TCT TCT AGA Thr Gln Lys Glu Glu Thr Glu Ser Gly Ser Gly Pro Lys Ser Ser Arg 375 380 385 390	1324
AAC ACA TTG GAA GCT GCG CTC AAT TCT ATT CGC TAC ATT ACA AGA CAC Asn Thr Leu Glu Ala Ala Leu Asn Ser Ile Arg Tyr Ile Thr Arg His 395 400 405	1372
ATC ATG AAG GAA AAT GAT GTC CGT GAG GTT GTT GAA GAT TGG AAA TTC Ile Met Lys Glu Asn Asp Val Arg Glu Val Val Glu Asp Trp Lys Phe 410 415 420	1420
ATA GCC CAG GTT CTT GAT CGG ATG TTT CTG TGG ACT TTT CTT TTC GTT Ile Ala Gln Val Leu Asp Arg Met Phe Leu Trp Thr Phe Leu Phe Val 425 430 435	1468
TCA ATT GTT GGA TCT CTT GGG CTT TTT GTT CCT GTT ATT TAT AAA TGG Ser Ile Val Gly Ser Leu Gly Leu Phe Val Pro Val Ile Tyr Lys Trp 440 445 450	1516
GCA AAT ATA TTA ATA CCA GTT CAT ATT GGA AAT GCA AAT AAG TGAAGCCTCC Ala Asn Ile Leu Ile Pro Val His Ile Gly Asn Ala Asn Lys 455 460 465	1568
CAAGGGACTG AAGTATACAT TTAGTTAACA CACATATATC TGATGGCACC TATAAAATTA	1628
TGAAAATGTA AGTTATGTGT TAAATTTAGT GCAAGCTTTA ACAGACTAAG TTGCTAACCT	1688
CAATTTATGT TAACAGATGA TCCATTTGAA CAGTTGGCTG TATGACTGAA GTAATAACTG	1748
ATGAGATACA TTTGATCTTG TAAAAATAGC AAAATATTAT CTGAAGTGA CTAGTGAAAA	1808
ATCTAGTATT TGTATCCTGG	1828

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein













Gln Trp Val Val Glu Asn Ser Glu His Ser Pro Glu Val Glu Asp Val  
420 425 430  
Ile Asn Ser Val Gln Phe Ile Ala Glu Asn Met Lys Ser His Asn Glu  
435 440 445  
Thr Lys Glu Val Glu Asp Asp Trp Lys Tyr Val Ala Met Val Val Asp  
450 455 460  
Arg Val Phe Leu Trp Val Phe Ile Ile Val Cys Val Phe Gly Thr Ala  
465 470 475 480  
Gly Leu Phe Leu Gln Pro Leu Leu Gly Asn Thr Gly Lys Ser  
485 490

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1876 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 73..1581
- (D) OTHER INFORMATION: /product= "ALPHA-7 SUBUNIT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGCCGCAGGC GCAGGCCCGG GCGACAGCCG AGACGTGGAG CGCGCCGGCT CGCTGCAGCT	60
CCGGGACTCA ACATGCGCTG CTCGCCGGA GCGCTCTGGC TGGCGCTGGC CGCGTCGCTC	120
CTGCACGTGT CCCTGCAAGG CGAGTTCCAG AGGAAGCTTT ACAAGGAGCT GGTCAAGAAC	180
TACAATCCCT TGGAGAGGCC CGTGGCCAAT GACTCGCAAC CACTCACCCT CTACTTCTCC	240
CTGAGCCTCC TGCAGATCAT GGACGTGGAT GAGAAGAACC AAGTTTTAAC CACCAACATT	300
TGGCTGCAAA TGTCTTGAC AGATCACTAT TTACAGTGA ATGTGTCAGA ATATCCAGGG	360
GTGAAGACTG TTCGTTTCCC AGATGGCCAG ATTGGAAC CAGACATTCT TCTCTATAAC	420
AGTGCTGATG AGCGCTTTGA CGCCACATTC CACACTAAG TGTGGTGAA TTCTTCTGGG	480
CATTGCCAGT ACCTGCCTCC AGGCATATTC AAGAGTTCTT GCTACATCGA TGTACGCTGG	540
TTCCCTTTG ATGTGCAGCA CTGCAAACTG AAGTTTGGGT CCTGGTCTTA CGGAGGCTGG	600
TCCTTGGATC TGCAGATGCA GGAGGCAGAT ATCAGTGGCT ATATCCCCAA TGGAGAATGG	660
GACCTAGTGG GAATCCCCGG CAAGAGGAGT GAAAGGTTCT ATGAGTGCTG CAAAGAGCCC	720
TACCCCGATG TCACCTTCAC AGTGACCATG CGCCGCAGGA CGCTCTACTA TGGCCTCAAC	780
CTGCTGATCC CCTGTGTGCT CATCTCCGCC CTCGCCCTGC TGGTGTTCCT GCTTCCTGCA	840
GATTCCGGGG AGAAGATTTC CCTGGGGATA ACAGTCTTAC TCTCTCTTAC CGTCTTCATG	900
CTGCTCGTGG CTGAGATCAT GCGCGCAACA TCCGATTCGG TACCATTGAT AGCCCGATAC	960
TTGCCAGCA CCATGATCAT CGTGGCCCTC TCGGTGGTGG TGACGGTGAT CGTGCTGCAG	1020

TACCACCACC ACGACCCCGA CGGGGGCAAG ATGCCCAAGT GGACCAGAGT CATCCTTCTG 1080  
AACTGGTGCG CGTGGTTCCT SCGAATGAAG AGSCCCGGGG AGGACAAGGT GCGCCCGGCC 1140  
TGCCAGCACA AGCAGCGGGC CTGCAGCCTG GCCAGTGTGG AGATGAGCGC CGTGGCGCCG 1200  
CCGCCCCGCCA GCAACGGGAA CCTGCTGTAC ATCGGCTTCC GCGGCCTGGA CGGCGTGCAC 1260  
TGTGTCCCGA CCCCCGACTC TGGGGTAGTG TGTGGCCGCA TGGCCTGCTC CCCCACGCAC 1320  
GATGAGCACC TCCTGCACGG CGGGCAACCC CCCGAGGGGG ACCCGGACTT GGCCAAGATC 1380  
CTGGAGGAGG TCCGCTACAT TGCCAATCGC TTCCGCTGCC AGGACGAAAG CGAGGCGGTC 1440  
TGCAGCGAGT GGAAGTTCGC CGCCTGTGTG GTGGACCGCC TGTGCCTCAT GGCCTTCTCG 1500  
GTCTTCACCA TCATCTGCAC CATCGGCATC CTGATGTCGG CTCCCAACTT CGTGGAGGCC 1560  
GTGTCCAAAG ACTTTGCGTA ACCACGCCTG GTTCTGTACA TGTGGAAAAC TCACAGATGG 1620  
GCAAGGCCTT TGGCTTGGCG AGATTTGGGG GTGCTAATCC AGGACAGCAT TACACGCCAC 1680  
AACTCCAGTG TTCCCTTCTG GCTGTCAGTC GTGTTGCTTA CGGTTTCTTT GTTACTTTAG 1740  
GTAGTAGAAT CTCAGCACTT TGTTCATAT TCTCAGATGG GCTGATAGAT ATCCTTGGCA 1800  
CATCCGTACC ATCGGTCAGC AGGGCCACTG AGTAGTCATT TTGCCCATTA GCCCACTGCC 1860  
TGGAAAGCCC TTCGGA 1876

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met	Arg	Cys	Ser	Pro	Gly	Gly	Val	Trp	Leu	Ala	Leu	Ala	Ala	Ser	Leu
1				5					10					15	
Leu	His	Val	Ser	Leu	Gln	Gly	Glu	Phe	Gln	Arg	Lys	Leu	Tyr	Lys	Glu
				20				25					30		
Leu	Val	Lys	Asn	Tyr	Asn	Pro	Leu	Glu	Arg	Pro	Val	Ala	Asn	Asp	Ser
				35			40					45			
Gln	Pro	Leu	Thr	Val	Tyr	Phe	Ser	Leu	Ser	Leu	Leu	Gln	Ile	Met	Asp
				50		55					60				
Val	Asp	Glu	Lys	Asn	Gln	Val	Leu	Thr	Thr	Asn	Ile	Trp	Leu	Gln	Met
				65		70				75				80	
Ser	Trp	Thr	Asp	His	Tyr	Leu	Gln	Trp	Asn	Val	Ser	Glu	Tyr	Pro	Gly
				85					90					95	
Val	Lys	Thr	Val	Arg	Phe	Pro	Asp	Gly	Gln	Ile	Trp	Lys	Pro	Asp	Ile
				100				105					110		
Leu	Leu	Tyr	Asn	Ser	Ala	Asp	Glu	Arg	Phe	Asp	Ala	Thr	Phe	His	Thr
				115			120					125			
Asn	Val	Leu	Val	Asn	Ser	Ser	Gly	His	Cys	Gln	Tyr	Leu	Pro	Pro	Gly
				130			135					140			



Val Ser Lys Asp Phe Ala  
500

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2448 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 265..1773
- (D) OTHER INFORMATION: /product= "BETA-2 SUBUNIT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CTCTCTCCCC TCACCGTCCC AATTGTATTC CCTGGAAGAG CAGCCGGAAA AGCCTCCGGC	60
TGCTCATACC AGGATAGGCA AGAAGCTGGT TTCTCCTCGC AGCCGGCTCC CTGAGGCCCA	120
GGAACCACCG CGGCGGCCCG CACCACCTGG ACCCAGCTCC AGGCGGGCGC GGCTTCAGCA	180
CCACGGACAG CGCCCCACCC GCGGCCCTCC CCCCGGCGGC GCGCTCCAGC CGGTGTAGGC	240
GAGGCAGCGA GCTATGCCCG CGGC ATG GCC CGG CGC TGC GGC CCC GTG GCG	291
Met Ala Arg Arg Cys Gly Pro Val Ala	
1 5	
CTG CTC CTT GGC TTC GGC CTC CTC CGG CTG TGC TCA GGG GTG TGG GGT	339
Leu Leu Leu Gly Phe Gly Leu Leu Arg Leu Cys Ser Gly Val Trp Gly	
10 15 20 25	
ACG GAT ACA GAG GAG CGG CTG GTG GAG CAT CTC CTG GAT CCT TCC CGC	387
Thr Asp Thr Glu Glu Arg Leu Val Glu His Leu Leu Asp Pro Ser Arg	
30 35 40	
TAC AAC AAG CTT ATC CGC CCA GCC ACC AAT GGC TCT GAG CTG GTG ACA	435
Tyr Asn Lys Leu Ile Arg Pro Ala Thr Asn Gly Ser Glu Leu Val Thr	
45 50 55	
GTA CAG CTT ATG GTG TCA CTG GCC CAG CTC ATC AGT GTG CAT GAG CGG	483
Val Gln Leu Met Val Ser Leu Ala Gln Leu Ile Ser Val His Glu Arg	
60 65 70	
GAG CAG ATC ATG ACC ACC AAT GTC TGG CTG ACC CAG GAG TGG GAA GAT	531
Glu Gln Ile Met Thr Thr Asn Val Trp Leu Thr Gln Glu Trp Glu Asp	
75 80 85	
TAT CGC CTC ACC TGG AAG CCT GAA GAG TTT GAC AAC ATG AAG AAA GTT	579
Tyr Arg Leu Thr Trp Lys Pro Glu Glu Phe Asp Asn Met Lys Lys Val	
90 95 100 105	
CGG CTC CCT TCC AAA CAC ATC TGG CTC CCA GAT GTG GTC CTG TAC AAC	627
Arg Leu Pro Ser Lys His Ile Trp Leu Pro Asp Val Val Leu Tyr Asn	
110 115 120	
AAT GCT GAC GGC ATG TAC GAG GTG TCC TTC TAT TCC AAT GCC GTG GTC	675
Asn Ala Asp Gly Met Tyr Glu Val Ser Phe Tyr Ser Asn Ala Val Val	
125 130 135	
TCC TAT GAT GGC AGC ATC TTC TGG CTG CCG CCT GCC ATC TAC AAG AGC	723
Ser Tyr Asp Gly Ser Ile Phe Trp Leu Pro Pro Ala Ile Tyr Lys Ser	
140 145 150	

GCA	TGC	AAG	ATT	GAA	GTA	AAG	CAC	TTC	CCA	TTT	GAC	CAG	CAG	AAC	TGC	771
Ala	Cys	Lys	Ile	Glu	Val	Lys	His	Phe	Pro	Phe	Asp	Gln	Gln	Asn	Cys	
155						160					165					
ACC	ATG	AAG	TTC	CGT	TCG	TGG	ACC	TAC	GAC	CGC	ACA	GAG	ATC	GAC	TTG	819
Thr	Met	Lys	Phe	Arg	Ser	Trp	Thr	Tyr	Asp	Arg	Thr	Glu	Ile	Asp	Leu	
170					175					180					185	
GTG	CTG	AAG	AGT	GAG	GTG	GCC	AGC	CTG	GAC	GAC	TTC	ACA	CCT	AGT	GGT	867
Val	Leu	Lys	Ser	Glu	Val	Ala	Ser	Leu	Asp	Asp	Phe	Thr	Pro	Ser	Gly	
				190					195					200		
GAG	TGG	GAC	ATC	GTG	GCG	CTG	CCG	GGC	CGG	CGC	AAC	GAG	AAC	CCC	GAC	915
Glu	Trp	Asp	Ile	Val	Ala	Leu	Pro	Gly	Arg	Arg	Asn	Glu	Asn	Pro	Asp	
			205					210						215		
GAC	TCT	ACG	TAC	GTG	GAC	ATC	ACG	TAT	GAC	TTC	ATC	ATT	CGC	CGC	AAG	963
Asp	Ser	Thr	Tyr	Val	Asp	Ile	Thr	Tyr	Asp	Phe	Ile	Ile	Arg	Arg	Lys	
		220					225					230				
CCG	CTC	TTC	TAC	ACC	ATC	AAC	CTC	ATC	ATC	CCC	TGT	GTG	CTC	ATC	ACC	1011
Pro	Leu	Phe	Tyr	Thr	Ile	Asn	Leu	Ile	Ile	Pro	Cys	Val	Leu	Ile	Thr	
		235				240					245					
TCG	CTA	GCC	ATC	CTT	GTC	TTC	TAC	CTG	CCA	TCC	GAC	TGT	GGC	GAG	AAG	1059
Ser	Leu	Ala	Ile	Leu	Val	Phe	Tyr	Leu	Pro	Ser	Asp	Cys	Gly	Glu	Lys	
250					255					260					265	
ATG	ACG	TTG	TGC	ATC	TCA	GTG	CTG	CTG	GCG	CTC	ACG	GTC	TTC	CTG	CTG	1107
Met	Thr	Leu	Cys	Ile	Ser	Val	Leu	Leu	Ala	Leu	Thr	Val	Phe	Leu	Leu	
				270					275					280		
CTC	ATC	TCC	AAG	ATC	GTG	CCT	CCC	ACC	TCC	CTC	GAC	GTG	CCG	CTC	GTC	1155
Leu	Ile	Ser	Lys	Ile	Val	Pro	Pro	Thr	Ser	Leu	Asp	Val	Pro	Leu	Val	
			285					290					295			
GGC	AAG	TAC	CTC	ATG	TTC	ACC	ATG	GTG	CTT	GTC	ACC	TTC	TCC	ATC	GTC	1203
Gly	Lys	Tyr	Leu	Met	Phe	Thr	Met	Val	Leu	Val	Thr	Phe	Ser	Ile	Val	
		300					305					310				
ACC	AGC	GTG	TGC	GTG	CTC	AAC	GTG	CAC	CAC	CGC	TCG	CCC	ACC	ACG	CAC	1251
Thr	Ser	Val	Cys	Val	Leu	Asn	Val	His	His	Arg	Ser	Pro	Thr	Thr	His	
		315				320					325					
ACC	ATG	GCG	CCC	TGG	GTG	AAG	GTC	GTC	TTC	CTG	GAG	AAG	CTG	CCC	GCG	1299
Thr	Met	Ala	Pro	Trp	Val	Lys	Val	Val	Phe	Leu	Glu	Lys	Leu	Pro	Ala	
330					335					340					345	
CTG	CTC	TTC	ATG	CAG	CAG	CCA	CGC	CAT	CAT	TGC	GCC	CGT	CAG	CGC	CTG	1347
Leu	Leu	Phe	Met	Gln	Gln	Pro	Arg	His	His	Cys	Ala	Arg	Gln	Arg	Leu	
				350				355						360		
CGC	CTG	CGG	CGA	CGC	CAG	CGT	GAG	CGC	GAG	GGC	GCT	GGA	GCC	CTC	TTC	1395
Arg	Leu	Arg	Arg	Arg	Gln	Arg	Glu	Arg	Glu	Gly	Ala	Gly	Ala	Leu	Phe	
			365					370					375			
TTC	CGC	GAA	GCC	CCA	GGG	GCC	GAC	TCC	TGC	ACG	TGC	TTC	GTC	AAC	CGC	1443
Phe	Arg	Glu	Ala	Pro	Gly	Ala	Asp	Ser	Cys	Thr	Cys	Phe	Val	Asn	Arg	
		380					385					390				
GCG	TCG	GTG	CAG	GGG	TTG	GCC	GGG	GCC	TTC	GGG	GCT	GAG	CCT	GCA	CCA	1491
Ala	Ser	Val	Gln	Gly	Leu	Ala	Gly	Ala	Phe	Gly	Ala	Glu	Pro	Ala	Pro	
		395				400					405					
GTG	GCG	GGC	CCC	GGG	CGC	TCA	GGG	GAG	CCG	TGT	GGC	TGT	GGC	CTC	CGG	1539
Val	Ala	Gly	Pro	Gly	Arg	Ser	Gly	Glu	Pro	Cys	Gly	Cys	Gly	Leu	Arg	
410					415					420					425	





Gly Glu Pro Cys Gly Cys Gly Leu Arg Glu Ala Val Asp Gly Val Arg  
                     420                    425                    430  
 Phe Ile Ala Asp His Met Arg Ser Glu Asp Asp Asp Gln Ser Val Ser  
                     435                    440                    445  
 Glu Asp Trp Lys Tyr Val Ala Met Val Ile Asp Arg Leu Phe Leu Trp  
                     450                    455                    460  
 Ile Phe Val Phe Val Cys Val Phe Gly Thr Ile Gly Met Phe Leu Gln  
                     465                    470                    475                    480  
 Pro Leu Phe Gln Asn Tyr Thr Thr Thr Thr Phe Leu His Ser Asp His  
                     485                    490                    495  
 Ser Ala Pro Ser Ser Lys  
                     500

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1927 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 98..1474
- (D) OTHER INFORMATION: /product= "BETA-3 SUBUNIT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TCGGAACCCC TGTATTTTCT TTTCAAACC CCCTTTTCCA GTGGAAATGC TCTGTTGTTA	60
AAAAGGAAGA AACTGTCTTT CTGAAACTGA CATCACG ATG CTC CCA GAT TTT ATG	115
Met Leu Pro Asp Phe Met	5
CTG GTT CTC ATC GTC CTT GGC ATC CCT TCC TCA GCC ACC ACA GGT TTC	163
Leu Val Leu Ile Val Leu Gly Ile Pro Ser Ser Ala Thr Thr Gly Phe	20
AAC TCA ATC GCC GAA AAT GAA GAT GCC CTC CTC AGA CAT TTG TTC CAA	211
Asn Ser Ile Ala Glu Asn Glu Asp Ala Leu Leu Arg His Leu Phe Gln	35
GGT TAT CAG AAA TGG GTC CGC CCT GTA TTA CAT TCT AAT GAC ACC ATA	259
Gly Tyr Gln Lys Trp Val Arg Pro Val Leu His Ser Asn Asp Thr Ile	50
AAA GTA TAT TTT GGA TTG AAA ATA TCC CAG CTT GTA GAT GTG GAT GAA	307
Lys Val Tyr Phe Gly Leu Lys Ile Ser Gln Leu Val Asp Val Asp Glu	70
AAG AAT CAG CTG ATG ACA ACC AAT GTG TGG CTC AAA CAG GAA TGG ACA	355
Lys Asn Gln Leu Met Thr Thr Asn Val Trp Leu Lys Gln Glu Trp Thr	85
GAC CAC AAG TTA CGC TGG AAT CCT GAT GAT TAT GGT GGG ATC CAT TCC	403
Asp His Lys Leu Arg Trp Asn Pro Asp Asp Tyr Gly Gly Ile His Ser	100







Ala Leu Lys Met Trp Leu His Ser Tyr His  
450 455

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1915 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 87..1583
- (D) OTHER INFORMATION: /product= "BETA-4 SUBUNIT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CCGGCGCTCA CTCGACCGCG CGGCTCACGG GTGCCCTGTG ACCCCACAGC GGAGCTCGCG	60
GCGGCTGCCA CCGGCCCCCG CCGGCCATGA GCGCGCGCGC TTCCCTGGTC CTTTCTCTCC	120
TGGTCGCCCT TTGCGGGCGC GGGAAGTGCC GCGTGCCAA TCGGAGGAA AAGCTGATGG	180
ACGACCTTCT GAACAAAACC CGTTACAATA ACCTGATCCG CCCAGCCACC AGCTCCTCAC	240
AGCTCATCTC CATCAAGCTG CAGCTCTCCC TGGCCAGCT TATCAGCGTG AATGAGCGAG	300
AGCAGATCAT GACCACCAAT GTCTGGCTGA AACAGGAATG GACTGATTAC CGCCTGACCT	360
GGAACAGCTC CCGCTACGAG GGTGTGAACA TCCTGAGGAT CCCTGCAAAG CGCATCTGGT	420
TGCCTGACAT CGTGCTTTAC AACAAACCGG ACGGGACCTA TGAGGTGTCT GTCTACACCA	480
ACTTGATAGT CCGGTCCAAC GGCAGCGTCC TGTGGCTGCC CCCTGCCATC TACAAGAGCG	540
CCTGCAAGAT TGAGGTGAAG TACTTTCCCT TCGACCAGCA GAACTGCACC CTCAAGTTCC	600
GCTCCTGGAC CTATGACCAC ACGGAGATAG ACATGGTCCT CATGACGCCC ACAGCCAGCA	660
TGGATGACTT TACTCCCAGT GGTGAGTGGG ACATAGTGGC CCTCCCAGGG AGAAGGACAG	720
TGAACCCACA AGACCCACG TACGTGGAGG TGAATTACGA CTTTCATC ATC AAGCGCAAGC	780
CTCTGTTCTA CACCATCAAC CTCATCATCC CCTGCGTGCT CACCACCTTG CTGGCCATCC	840
TCGTCTTCTA CCTGCCATCC GACTGCGGCG AGAAGATGAC ACTGTGCATC TCAGTGCTGC	900
TGGCACTGAC ATTCTTCCTG CTGCTCATCT CCAAGATCGT GCCACCCACC TCCCTCGATG	960
TGCCTCTCAT CGGCAAGTAC CTCATGTTCA CCATGGTGCT GGTCACTTC TCCATCGTCA	1020
CCAGCGTCTG TGTGCTCAAT GTGCACCACC GCTCGCCCAG CACCCACACC ATGGCACCCCT	1080
GGGTCAAGCG CTGCTTCCTG CACAAGCTGC CTACCTTCCT CTTTCATGAAG CGCCCTGGCC	1140
CCGACAGCAG CCGGCCCCAG GCCTTCCCGC CCAGCAAGTC ATGGGTGACC AAGCCCGAGG	1200
CCACCGCCAC CTCCACCAGC CCCTCCAAC TCTATGGGAA CTCCATGTAC TTTGTGAACC	1260
CCGCTCTGCG AGCTTCCAAG TCTCCAGCCG GCTCTACCCC GGTGGCTATC CCCAGGGATT	1320
TCTGGCTGCG GTCTCTGGG AGGTTCCGAC AGGATGTGCA GGAGGCATTA GAAGGTGTCA	1380

Year	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 498 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met 1	Arg	Arg	Ala 5	Pro	Ser	Leu	Val	Leu 10	Phe	Leu	Val	Ala 15	Leu	Cys
Gly	Arg	Gly	Asn 20	Cys	Arg	Val	Ala	Asn 25	Ala	Glu	Glu	Lys 30	Leu	Met Asp
Asp	Leu	Leu 35	Asn	Lys	Thr	Arg	Tyr 40	Asn	Asn	Leu	Ile	Arg 45	Pro	Ala Thr
Ser	Ser 50	Ser	Gln	Leu	Ile	Ser 55	Ile	Lys	Leu	Gln	Leu 60	Ser	Leu	Ala Gln
Leu 65	Ile	Ser	Val	Asn	Glu 70	Arg	Glu	Gln	Ile	Met 75	Thr	Thr	Asn	Val Trp 80
Leu	Lys	Gln	Glu	Trp 85	Thr	Asp	Tyr	Arg	Leu 90	Thr	Trp	Asn	Ser	Ser Arg 95
Tyr	Glu	Gly	Val 100	Asn	Ile	Leu	Arg	Ile 105	Pro	Ala	Lys	Arg	Ile 110	Trp Leu
Pro	Asp	Ile 115	Val	Leu	Tyr	Asn 120	Asn	Ala	Asp	Gly	Thr	Tyr 125	Glu	Val Ser
Val	Tyr 130	Thr	Asn	Leu	Ile	Val 135	Arg	Ser	Asn	Gly	Ser 140	Val	Leu	Trp Leu
Pro 145	Pro	Ala	Ile	Tyr	Lys 150	Ser	Ala	Cys	Lys	Ile 155	Glu	Val	Lys	Tyr Phe 160
Pro	Phe	Asp	Gln 165	Gln	Asn	Cys	Thr	Leu	Lys 170	Phe	Arg	Ser	Trp	Thr Tyr 175
Asp	His	Thr	Glu 180	Ile	Asp	Met	Val	Leu 185	Met	Thr	Pro	Thr	Ala	Ser Met 190
Asp	Asp	Phe 195	Thr	Pro	Ser	Gly	Glu 200	Trp	Asp	Ile	Val	Ala 205	Leu	Pro Gly





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